

GenCore version 5.1.3
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OM protein - protein search, using sw model
Run on: November 30, 2002, 12:23:18 ; Search time 57.9734 seconds
Scoring table: BLOSUM62 (without alignments)
Gapop 10.0 , Gapext 0.5
Searched: 671580 seqs, 20647115 residues
Total number of hits satisfying chosen parameters: 671580
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPREMBL_21:
1: sp_archea:/*
2: sp_bacteria:/*
3: sp_fungi:/*
4: sp_human:/*
5: sp_invertebrate:/*
6: sp_mammal:/*
7: sp_minc:/*
8: sp_organelle:/*
9: sp_phage:/*
10: sp_plant:/*
11: sp_rabbit:/*
12: sp_rabbit:/*
13: sp_vertebrate:/*
14: sp_unclassified:/*
15: sp_virus:/*
16: sp_bacteria:/*
17: sp_archeap:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
ID Q96QG1 PRELIMINARY; PRT; 924 AA.
AC Q96QG1; 01-DEC-2001 (TRMBLrel. 19, Created)
DT 01-DEC-2001 (TRMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TRMBLrel. 21, Last annotation update)
DE Sodium/calcium exchanger SCL8A3.
GN SCL8A3.
OS Homo sapiens (Human). Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butherea; Primates; Catarrhini; Hominidae; Homo.
OC NCBITaxID=9606;
OX [1]
RN RP
RA SEQUENCE FROM N.A.
RA Bortoluzzi S.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA
RA
RT "Characterization of the human SCL8A3 gene for solute carrier family 8, member 3 (sodium/calcium exchanger).";
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RL DR
DR EMBL; AU304853; CAC40985.1;
DR Intertro; IPR005644; Ca1x_beta.
DR Intertro; IPR004837; NaCa_Exbeta.
DR Intertro; IPR004836; NaCa_Ex.
DR Pfam; PF03160; Ca1x_beta; 2.
DR Pfam; PF01699; Na_Ca_Ex; 2.
DR TIGRFAMs; TIGR00845; caca_1.
DR TIGRFAMs; TIGR00845; caca_1.
SQ SEQUENCE; 924 AA; 102694 MW; A0A556B753998A07 CRC64;
Query Match 99.4%; Score 4768.5; DB 4; Length 924;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 918; Conservative 1; Mismatches 2; Index 3; Gaps 1;

Qy 1 MAWLRLQPLTSFLHRLGLVTFVFLNGLRATAGGSDVPSITGQNNESSCSDCKEGVIL 60
Db 1 MAWLRLQPLTSFLHRLGLVTFVFLNGLRATAGGSDVPSITGQNNESSCSDCKEGVIL 60
045630 caenorhabdi

QY	51	PINWPENPSLGDKARVIVYFVALIMLGVSIAIDRMASIEVITSOREVTKPNE	120	OC
Db	61	PIWYPENPSLGDKARVIVYFVALIMLGVSIAIDRMASIEVITSOREVTKPNE	120	NCB_ TaxID=906;
Db	121	TSTTIRWNETVSNTLMALGSSAPEILLSIEVCGGHFTIADLRPTIVSAAFNMF	180	RN [1]
Db	181	IIIGCIVVYIPDGTRKIKHLRVEFTAWSIAYIWIMLAVFSPGVQWEGLTLFF	240	SEQUENCE FROM N.A.
Db	241	FPCVLLAWADRRLFYKMHKRYDKHGTIETEGDHPKIEMGKMMNSHFLDG	300	RA Borcoluzzi S.;
Db	241	FPCVLLAWADRRLFYKMHKRYDKHGTIETEGDHPKIEMGKMMNSHFLDG	300	RA Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
QY	301	LVPLEGKEDSERREMTRILDKLQKHPKEDDOLVEMANYVALSHQOKSRAFYRQATR	360	RN [2]
Db	301	LVPLEGKEDSERREMTRILDKLQKHPKEDDOLVEMANYVALSHQOKSRAFYRQATR	360	RA SEQUENCE FROM N.A.
Db	361	MMTGAGNITLKKHAEQAKASSMEVHDEPEFISKVFDPSYCQCLENGAVLTVR	420	RA Gazzellini N.;
Db	361	MMTGAGNITLKKHAEQAKASSMEVHDEPEFISKVFDPSYCQCLENGAVLTVR	420	RA "Characterization of the human SCL8A3 gene for solute carrier family
Db	421	KGGDSKMYVYDVKTEDGSANAGADYEETEGTVLKGOTREFSGVGLIDDEEDEHF	480	RT 8, member 3 (sodium/calcium exchanger).";
Db	421	KGGDSKMYVYDVKTEDGSANAGADYEETEGTVLKGOTREFSGVGLIDDEEDEHF	480	RT Submitted (2001) to the EMBL/GenBank/DBJ databases.
QY	481	FVRLSNRTEEPEEGMPATFNSLPLRAVIALSPCVATVTLDDDHAGIFTPECOMH	540	RL DR
Db	481	FVRLSNRTEEPEEGMPATFNSLPLRAVIALSPCVATVTLDDDHAGIFTPECOMH	540	EMBL; AT304052; CAC40984.1; -
QY	541	VSSIGMVWVKVLTSGARGTVVPERFVEGTAKGGDFEDYGELEFFKNDETVKTR	600	DR InterPro; IPR00364; Calx beta.
Db	541	VSSIGMVWVKVLTSGARGTVVPERFVEGTAKGGDFEDYGELEFFKNDETVKTR	600	DR InterPro; IPR004837; Na_Ca_Ex.
QY	601	KIVDEEEVERQENFFALGEPKMERGSDV---TKRLTMEEEAKRAMEKGKPVLG	657	DR Pfam; PF03160; Calx-beta; 2.
Db	601	KIVDEEEVERQENFFALGEPKMERGSDV---TKRLTMEEEAKRAMEKGKPVLG	657	DR TIGRFAMS; TIGR00845; eaca_1.
Db	601	KIVDEEEVERQENFFALGEPKMERGSDV---TKRLTMEEEAKRAMEKGKPVLG	657	DR SEQUENCE 925 AA; 102803 MW; OCFBDA0881C4FDA CRC64;
QY	658	PKLEVITTEESYERFTVDKLKLITNLALVGTHSWRQDFMEAITVSAGDEDDESGER	717	Query Match 97.4%; Score 4571; DB 4; Length 925;
Db	658	PKLEVITTEESYERFTVDKLKLITNLALVGTHSWRQDFMEAITVSAGDEDDESGER	717	Best Local Similarity 96.9%; Pred. No. 0; Mismatches 14; Indels 4; Gaps
Db	661	PKLEVITTEESYERFTVDKLKLITNLALVGTHSWRQDFMEAITVSAGDEDDESGER	720	Matches 896; Conservative 11; Mismatches 14; Indels 4; Gaps
Db	718	LPSCDFYVWHLFELVWKFIFACVPPTECHGWCFAVSLITGMITAIGDASHRCTI	777	Db 61 PIWYPENPSLGDKARVIVYFVALIMLGVSIAIDRMASIEVITSOREVTKPNE
Db	721	LPSCDFYVWHLFELVWKFIFACVPPTECHGWCFAVSLITGMITAIGDASHRCTI	780	120 121 TSTTIRWNETVSNTLMALGSSAPEILLSIEVCGGHFTIADLRPTIVSAAFNMF
QY	778	GLKDSVTVWVFAVGTSPDEPSKAALQDQYADASIGNVGSNAWVFLGLAWSA	837	QY 181 IIIGCIVVYIPDGTRKIKHLRVEFTAWSIAYIWIMLAVFSPGVQWEGLTLFF
Db	781	GLKDSVTVWVFAVGTSPDEPSKAALQDQYADASIGNVGSNAWVFLGLAWSA	840	Db 181 IIIGCIVVYIPDGTRKIKHLRVEFTAWSIAYIWIMLAVFSPGVQWEGLTLFF
QY	838	ATWALQGQEFHVSAGTFLAFSVLFTAFVCSVLLYRRPHIGGELGPRCKLATTW	897	QY 241 FPCVLLAWADRRLFYKMHKRYDKHGTIETEGDHPKIEMGKMMNSHFLDG
Db	841	ATWALQGQEFHVSAGTFLAFSVLFTAFVCSVLLYRRPHIGGELGPRCKLATTW	900	300 301 LVPLEGKEDSERREMTRILDKLQKHPKEDDOLVEMANYVALSHQOKSRAFYRQATR
QY	898	LFVSLWLYLFATLEAVCYING	921	360 241 FPCVLLAWADRRLFYKMHKRYDKHGTIETEGDHPKIEMGKMMNSHFLDG
Db	901	LFVSLWLYLFATLEAVCYING	924	420 361 MMTGAGNITLKKHAEQAKASSMEVHDEPEFISKVFDPSYCQCLENGAVLTVR
OS				420 361 MMTGAGNITLKKHAEQAKASSMEVHDEPEFISKVFDPSYCQCLENGAVLTVR
	RESULT 2			420 361 MMTGAGNITLKKHAEQAKASSMEVHDEPEFISKVFDPSYCQCLENGAVLTVR
096QG2				420 361 MMTGAGNITLKKHAEQAKASSMEVHDEPEFISKVFDPSYCQCLENGAVLTVR
ID	096QG2	PRELIMINARY;	PRY;	420 361 MMTGAGNITLKKHAEQAKASSMEVHDEPEFISKVFDPSYCQCLENGAVLTVR
AC	096QG2;			420 361 MMTGAGNITLKKHAEQAKASSMEVHDEPEFISKVFDPSYCQCLENGAVLTVR
DT	01-DEC-2001 (TREMble, 19, Created)			420 361 MMTGAGNITLKKHAEQAKASSMEVHDEPEFISKVFDPSYCQCLENGAVLTVR
DT	01-DEC-2001 (TREMble, 19, Last sequence update)			420 361 MMTGAGNITLKKHAEQAKASSMEVHDEPEFISKVFDPSYCQCLENGAVLTVR
DT	01-JUN-2002 (TREMble, 21, Last annotation update)			420 361 MMTGAGNITLKKHAEQAKASSMEVHDEPEFISKVFDPSYCQCLENGAVLTVR
DE	Sodium/calcium exchanger	SC18A3.		420 361 MMTGAGNITLKKHAEQAKASSMEVHDEPEFISKVFDPSYCQCLENGAVLTVR
GN	SC18A3.			420 361 MMTGAGNITLKKHAEQAKASSMEVHDEPEFISKVFDPSYCQCLENGAVLTVR
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			420 361 MMTGAGNITLKKHAEQAKASSMEVHDEPEFISKVFDPSYCQCLENGAVLTVR

QY	717	RLPSCDYWMELTIVFWKVLIFACVPPTEYCHGWCFAVSILIGMATAIGDLASHFGCT	776
Db	721	RLPSCDYWMELTIVFWKVLIFACVPPTEYCHGWCFAVSILIGMATAIGDLASHFGCT	780
Db	777	IGLKDSVTAVVFAFGTSVPDTFASKAALQDVADASIGNVTGSNAVNFLIGLGSV	836
Db	781	IGLKDSVTAVVFAFGTSVPDTFASKAALQDVADASIGNVTGSNAVNFLIGLGSV	840
QY	837	AAIYRALQGEFHVSAGTAFSFTLTFIFAVFCISVLLYRRPHLGGPRGCKLATT	895
Db	841	AAIYRALQGEFHVSAGTAFSFTLTFIFAVFCISVLLYRRPHLGGPRGCKLATT	900
Db	897	WLFVSIWLLYLIFATLEACYIKGF	921
QY	901	WLFVSIWLLYLIFATLEACYIKGF	925
RESULT	3		
QY	08VH08	PRELIMINARY;	PRT;
AC	08VH08;		928 AA.
AC	01-MAR-2002 (TREMBlrel. 20, Created)		
DT	01-MAR-2002 (TREMBlrel. 20, Last sequence update)		
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)		
DE	Sodium/calcium exchanger.		
GN	SLC8A3.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_Taxid=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CC57BL/6J; TISSUE=SKELETAL MUSCLE;		
RA	Kraev A.;		
RT	"Towards complete inventory of calcium transporters of the house mouse.", submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.		
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF0453257; AAL39160.1; -.		
DR	MGD; MGI:107976; SLC8a3.		
DR	InterPro; IPR00644; Calx.beta.		
DR	InterPro; IPR004837; Na_Ca_Exemb.		
DR	InterPro; IPR004836; Na_Ca_Ex.		
DR	Pfam; PF01699; Na_Ca_Ex; 2.		
DR	PRINTS; PRO1259; NACBXCHNR.		
DR	SEQUENCE: SM00237; Calx.beta; 2.		
DR	TIGRFRMS; TIGR00845; caca; 1.		
QO	SEQUENCE: 928 AA; 102943 MW; A36BBB30EE4123C0 CRC64;		
Query	Match	95.1%; Score 4563.5;	DB 11; Length 928;
Best	Local Similarity	94.2%; Pred. No. 0;	
Matches	874; Conservative	21; Mismatches	26; Indels 7; Gaps 1;
QY	1	MAWLRLQPLTSAFLHRLGVLTVFLNLGLRLEAGGSGDVPTGONNECSGSSOCKEGYL	60
Db	1	MAWLRLQPLTSAFLHRLGVLTVFLNLGLRLEAGGSGDVPTGONNECSGSSOCKEGYL	60
Db	1	MAWLRLQPLTSAFLHRLGVLTVFLNLGLRLEAGGSGDVPTGONNECSGSSOCKEGYL	60
QY	61	PIWYPPENPLSGDKIARVIVYFVALIYKFLGVSIADRMASIEVITSQEREVITKKPNE	120
Db	61	PIWYPPENPLSGDKIARVIVYFVALIYKFLGVSIADRMASIEVITSQEREVITKKPNE	120
QY	181	IGICGVVPIPOGETRKHLRFITAAWSIAYIWLMILAVFSPGTVQWIGLTLF	240
Db	181	IGICGVVPIPOGETRKHLRFITAAWSIAYIWLMILAVFSPGTVQWIGLTLF	240
QY	181	IGICGVVPIPOGETRKHLRFITAAWSIAYIWLMILAVFSPGTVQWIGLTLF	240
Db	181	IGICGVVPIPOGETRKHLRFITAAWSIAYIWLMILAVFSPGTVQWIGLTLF	240
QY	121	TTTTTRVWNETVSNITLMAKGSSAPEPLS1TEVCGHGIAQDGLGPSTIVGSAFNMT	180
Db	121	TTTTTRVWNETVSNITLMAKGSSAPEPLS1TEVCGHGIAQDGLGPSTIVGSAFNMT	180
QY	181	IGICGVVPIPOGETRKHLRFITAAWSIAYIWLMILAVFSPGTVQWIGLTLF	240
Db	181	IGICGVVPIPOGETRKHLRFITAAWSIAYIWLMILAVFSPGTVQWIGLTLF	240
QY	181	IGICGVVPIPOGETRKHLRFITAAWSIAYIWLMILAVFSPGTVQWIGLTLF	240
Db	181	IGICGVVPIPOGETRKHLRFITAAWSIAYIWLMILAVFSPGTVQWIGLTLF	240
QY	241	FPVCVLLAWWADKRLYKYMKKYRDKHGTIEEGDHPKIEMDGKMMNSHLDGN	300
QY	241	FPVCVLLAWWADKRLYKYMKKYRDKHGTIEEGDHPKIEMDGKMMNSHLDGN	300
QY	241	FPVCVLLAWWADKRLYKYMKKYRDKHGTIEEGDHPKIEMDGKMMNSHLDGN	300

DR	PRINTS: PRO01259; NACAECHNGR.	RESULT 5
DR	SMART; SM00237; Calx_beta; 2.	Q28662
DR	TIGRFAMS; TIGR00045; caca; 1.	PRELIMINARY; PRT; 941 AA.
DR	PROSITE: PS0076; DN AJ 2; 1.	ID Q28662; AC
SEQUENCE	934 AA; 104331 MW; 2A228DA30254BBC2 CRC64;	028662; 028662; 01-NOV-1996 (TREMBLrel. 01, Created)
Qy	1 MAWLRLOPLTSRHLFCLVTFVFL- LNGLRAEGSGDV STGQNNECSGSSDCKEV 58	DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
Db	1 MRRLSLSPTESMGCFHLVIVALFSHVYVIA TEMEGEGNETGE -- CUGSYCKKG 56	DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
Qy	59 ILPIWYENPSIGDKIARVIV VFVALYMEGLGVSIADRFMASEIVT SOEREVTKPN 118	DE Renal Na/Ca exchanger NACA-2.
Qy	117 GETKTVRINNETVSNELMAGLSSAPEILISVIEVGHNFTAGDLGPSTIVGSAFM 176	GN NCX1.
Db	57 ILPIWERQDPSRGDKIARATVYFVANVYMFGLGVSIADRFMSSIEVTSQEKEITKKPN 116	OS Oryctolagus cuniculus (Rabbit).
Qy	119 GEMSTTIVRWHETVSNELMAGLSSAPEILISLIEVGHGFTAGDLGPSTIVGSAFM 178	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Qy	119 GEMSTTIVRWHETVSNELMAGLSSAPEILISLIEVGHGFTAGDLGPSTIVGSAFM 178	OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
Db	117 GETKTVRINNETVSNELMAGLSSAPEILISVIEVGHNFTAGDLGPSTIVGSAFM 176	OX NCBI TaxID=9986;
179	FLIGICVYVWGETKIKHARFETAAMSIFAYIWLYMLAVSPGVWQWEGILTL 238	[1] RN
Db	177 FLITALCVVWVPG DETRKIKHLRVEF TAASIFAYTWLYTILLSVISP PGVVEW EGILTL 236	SEQUENCE FROM N.A.
Qy	239 FPFPCVCLLAWADKRLFYKWHKKYRDTKDRGKLTTEG DHKG --IEMGKMMNH 295	RC TISSUE-KIDNEY;
Db	237 FPFPCVCFWADRLFYKVRAGKQRMIEHEDGRPSKTEIEMDGKVWNH 296	RC
Qy	296 --FLDNLVLPAGEKEND--ESRREMTRLDKLQKHPEDDOLVEMANYALSHQO 348	RX MEDLINE=92221271; PubMed=1621815;
Db	297 VENFLDGALV LEVDERQDDEBARREMARILKELKQKHPKEKEIOLIELANYQVLQQ 355	RA Reilly R.F.; Shngrue C.A.;
Qy	349 KSRAYFRIQATRM TGAGN IKKHAQAKYASMSVHTEPE- DFISKVFF PCSYQ 407	RA "CDNA cloning of a renal Na(+)–Ca2+ exchanger. ";
Db	356 KSRAYFRIQATRMLTGA GN IKRHAQDQKAVSMHEVNTEVEENDPVSKIFFEGNYQ 415	RA Am. J. Physiol. 262:F105-F109(1992).
Qy	408 LENCGAVLLTVRKGGDSKTMVYDVKTEDGSA NAGADYE TEGTWVLPKG ETOK ESVG 467	[2] RN
Db	416 LENCGTVALTIRGGDLTWVFRDFTEDGTAA NGSDV E TEGT WVFK GET OKIRVG 475	SEQUENCE FROM N.A.
Qy	468 IIDDDEPEDEHFPVRSNVRREEPEEGMPATFNSLPLPRAVIA SPCVAT VTLDD 527	RC TISSUE-KIDNEY;
Db	476 IIDDDEPEDEHFPVRSNVRREEPEEGMPATFNSLPLPRAVIA SPCVAT VTLDD 532	RA Reilly R.F.; Shngrue C.A.;
Qy	528 HAGI FECDT TV SE SGVMEVKV RTG RTG TV W PF RT VEG TAKGGD FE DY GE L 587	RA Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
Db	533 HAGI FECDT TV SE SGVMEVKV RTG RTG TV W PF RT VEG TAKGGD FE DY GE L 592	DR EMBL: U52665; AAQ97928; 1. -
Qy	588 EFKND EVTK TV SE YEF TV KV IDE EE ER Q EN F IA GE K MM ER G---ISD V DRK--LT ME 639	DR IntePro; IPR03644; Calx_beta.
Db	593 ERQND EVTK IT TR FE EE KE CS PL VE PKW IR RG KG FF IT DE DD Q PL TSK 652	DR InterPro; IPR04837; NacA_Exemb.
Qy	640 EERAKRAEMGKPV GL HP K LEV IE YEF T VK L IK N LA V GT IS W D ME 699	DR InterPro; IPR04836; Na_Ca_Ex.
Db	653 EEEERR IA EMG R FL G HT E KT K LEV IE YEF T VK L IK N LA V GT IS W D ME 712	DR Pfam; PF03160; Calx_beta; 2.
Qy	700 ITVSAGADEDESE GE R LP SC DF Y HM FL FC TV CH GW AC FA VI L 759	DR Pfam; PF01699; Na_Ca_Ex; 2.
Db	713 ITVSAGEDDD DC GE GE K LP SC DF Y HM FL FC TV CH GW AC FA VI L 772	DR SMART; SM00237; Calx_beta; 1.
Qy	760 GMLTAIGD L ASH F G C T G IK D ST A V V FA G T S P D F A SK A Q L D V A D S A G N T 819	DR TIGRFAMS; TIGR00045; caca; 1.
Qy	773 GLLTAF G DL AS H F G C T G IK D ST A V V FA G T S P D F A SK A Q L D V A D S A G N T 832	Db 9 PMSGM F HL A VAL F FRD V SA E TE M E G E G N E T G 64
Qy	820 GSNAVN F LG C LAWS A Y W Q O EF H S A G T IA F VL T IF C V S U L X R RRP 879	Qy 127 RWNEV SN LT M AG S APE IL LS L IE V CG F ING D LS P ST I VG S AA N MF L IG C V 186
Db	833 GSNAVN F LG C LAWS A Y W Q O EF H S A G T IA F VL T IF C V S U L X R RRP 892	Db 125 RWNET SN LT M AG S APE IL LS L IE V CG F ING D LS P ST I VG S AA N MF L IG C V 184
Qy	880 HLG GE LG G PR C KL A T W LF S W L Y I LF T LE A Y C I Y IK G 921	Db 125 RWNET SN LT M AG S APE IL LS L IE V CG F ING D LS P ST I VG S AA N MF L IG C V 184
Db	893 EIG E LG G PR C KL A T W LF S W L Y I LF T LE A Y C I Y IK G 934	Db 247 LAW A DK R LL K Y M KK R D K HT E TE G D H K --IEMGKMMNH--FLDG 300
Qy		Db 245 FAW A DR R LL K Y M KK R D K HT E TE G D H K --IEMGKMMNH--FLDG 304
Db		Qy 301 LY P LE G E V D Y --ESR R MI L DK K Q K HP E KD P D Q L E Y M AN Y AL S Q R Y F 356
Qy		Db 305 LY-LD Y DER D D D E E AR M AR I LK E LP K Q K HP E K E OL I EL A NY Q V L SO O OK S RA F Y R 363
Qy		Db 357 QAT R MT G AG N IL K KK A E Q K A K S SE V T D E P -DF S KV F DP C S Y Q C LEN G A V I 415
Db		Db 364 QAT R MT G AG N IL K KK A E Q K A K S SE V T D E P -DF S KV F DP C S Y Q C LEN G A V I 423
Qy		Qy 416 LT V R K GG D MS K T M V D Y K T E D G S A N G AD E F E T C T V L K P G E T Q E R S V G I D D I F E 475

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCB1_TAXID=10116;
 RN [1]
 SEQUENCE FROM N.A.
 STRAIN=DRL/RAPP R SPRAGUE-DAWLEY;
 RA UniProt M.T., Bell, P.D.;
 RT "cDNA cloning of two Na+/Ca2+ exchangers in mesangial cells from Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats.", from
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF0109163; ADD23066; 1; --.
 DR InterPro: IPR03649; Calx_beta.
 DR InterPro: IPR01623; DnaJ_N.
 DR SMART: SM00237; Calx_beta; 2.
 DR TIGRFAMS: TIGR00845; caca; 1.
 DR PROSITE: PS50076; DNAl_2; 1.
 DR SEQUENCE 934 AA; 104166 MW; C04E0D8A75633DDC CRC64;

Query Match 71.5%; Score 3427.5; DB 11; Length 934;
 Best Local Similarity 70.9%; Pred. No. 5.8e-242;
 Matches 671; Conservative 107; Mismatches 127; Indels 41; Gaps 11;
 QY 4 LRRQPLTSALHLGLVLTFL-----NGLRAEAGGSDVPGSTQNNESCGSSDCK 55
 |||| :|| ||| :|| ||| | | ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| |||
 Db 2 LRLSLPPNVSMGRLVLTVALLEFLTHVHDHTADTEAEGGN-----ETEBCGSYCK 53
 QY 56 EGVILPPIWYPPENSLGKIAIRVIVYFVALYIMFLGVSTIADRMSSIEVTSQERVTIK 115
 |||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| |||
 Db 54 KGVILPWPQDPSFGDKIARATVYFVANVYMLGVSLIADRMSSIEVTSQERVTIK 113
 QY 116 KPGNGETSTTIRWNETVSNLTMALGSSAPELLSIEVCGHGFAGDLSSTVGSAA 175
 |||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| |||
 Db 114 KPGNGETTAKTIVRWTWNETVSNLTMALGSSAPELLSIEVCGHNFATAGDLSSTVGSAA 173
 QY 176 FNNFIIIGICVYVYIPDGTRKIKHLRPFITAAWSIAYIWLMLAVFSPGVQVOWEGL 235
 |||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| |||
 Db 174 FNNFIIIGICVYVYIPDGTRKIKHLRPFITAAWSIAYTWWLILSVSPGVVWEGL 233
 QY 236 LTFPFPPCIVVLLAWADRRLFLFKYVVKYRAGKQGMIEHEDRPAKSTEIEMDGKV 292
 |||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| |||
 Db 234 LTFPFPPCIVVLLAWADRRLFLFKYVVKYRAGKQGMIEHEDRPAKSTEIEMDGKV 293
 QY 293 NSI---FLDGNLWPLEGKEVD---ESREMRITILKOKHPEKDIDOLVEMANYAL 345
 |||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| |||
 Db 294 NSIHDNFIDGALY-LEVDERQDDEARREMARKILKELKOKHPEKDIDOLVEMANYAL 352
 QY 346 HQQKSRAFYRQIQTTRMMTGAAGNLLKHAEQAKKASSHEVTHDEPE-DFLSKVFFDPCS 404
 |||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| |||
 Db 353 QQQSKSRAFYRQIQTTRMMTGAAGNLLKHAEQAKKASSHEVTHDEPE-DFLSKVFFDPCS 412
 QY 405 YQOLENGAVLITVVKGGDMSTMYQKTEGDSANAGADBFTEGIVVLUKEGETOREF 464
 |||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| |||
 Db 413 YQOLENGAVLITVVKGGDMSTMYQKTEGDSANAGADBFTEGIVVLUKEGETOREF 472
 QY 465 SVVIIIDDDIFEEDEHFRVLSNRNTRIEBOPERGMPAPFNSFLPLR-AVLASPCVAVTI 523
 |||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| |||
 Db 473 RVGJIDDDIFEEDEHFRVLSNRVSVSSESDG---ILDSNHSVATACLSSPNTATTI 528
 QY 584 YGSELEFKNDETVTRVKVDEEYERQENPFLGKWMERGI-----SDVTDRK- 635
 |||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| |||
 Db 589 CGELEFQDNEIWKWITIRIFDREYEKECSFSVLSLEEPKWRKRGKGFTLIEYDKQP 648
 QY 636 LNEEEEEKRILAMGKPVLGHEPKLEVITEESEFKTVDKIKKTLALVYGHWSRDQ 695
 |||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| |||
 Db 649 LTKKEEEERRIAANGRPLGEHTKLEVITEESEYEFKSTVDKLUKKTNLALVYGTNSREQ 708

RESULT 8
 Q9WU30 ID Q9WU30 PRELIMINARY; PRNT; 934 AA.
 AC Q9WU30; DT 01-NOV-1999 (TREMBLR. 12, Created)
 DT 01-NOV-1999 (TREMBLR. 12, Last sequence update)
 DE Na+/Ca2+-exchanging protein.
 OS Rattus norvegicus (Rat).
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCB1_TAXID=10116;
 RN [1]
 SEQUENCE FROM N.A.
 STRAIN=SPRAGUE-DAWLEY;
 RA UniProt M.T., Bell, P.D.;
 RT "cDNA cloning of two Na+/Ca2+ exchangers in mesangial cells from Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats.", from
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF0109166; ADD23089; 1; --.
 DR InterPro: IPR03644; Calx_beta.
 DR InterPro: IPR01623; DnaJ_N.
 DR SMART: SM00237; Calx_beta; 2.
 DR TIGRFAMS: TIGR00845; caca; 1.
 DR PROSITE: PS50076; DNAl_2; 1.
 DR SEQUENCE 934 AA; 104210 MW; 054D06E917909B5 CRC64;

Query Match 71.4%; Score 3425.5; DB 11; Length 934;
 Best Local Similarity 70.8%; Pred. No. 8.2e-242;
 Matches 670; Conservative 108; Mismatches 127; Indels 41; Gaps 11;
 QY 4 LRRQPLTSALHLGLVLTFL-----NGLRAEAGGSDVPGSTQNNESCGSSDCK 55
 |||| :|| ||| :|| ||| | | ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| |||
 Db 2 LRLSLPPNVSMGRLVLTVALLEFLTHVHDHTADTEAEGGN-----ETEBCGSYCK 53
 QY 56 EGVILPPIWYPPENSLGKIAIRVIVYFVALYIMFLGVSTIADRMSSIEVTSQERVTIK 115
 |||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| |||
 Db 54 KGVILPWPQDPSFGDKIARATVYFVANVYMLGVSLIADRMSSIEVTSQERVTIK 113
 QY 176 FNNFIIIGICVYVYIPDGTRKIKHLRPFITAAWSIAYIWLMLAVFSPGVQVOWEGL 235
 |||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| |||
 Db 174 FNNFIIIGICVYVYIPDGTRKIKHLRPFITAAWSIAYTWWLILSVSPGVVWEGL 233
 QY 236 LTFPFPPCIVVLLAWADRRLFLFKYVVKYRAGKQGMIEHEDRPAKSTEIEMDGKV 292
 |||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| ||| :|| |||

293	NSH--FLOGNLVPLEGKEDM---ESREMIRTKDKOKHPEKDQDOLIVEANYALS	345	DR
294	NSHVDNFNLGALV-LEVDERDODEEARREMARTILKELKOKHPDKETBOLIELANYOVL	352	DR
346	HQKSRAFYRIQATRMMTGAGNIKKHAAEQAKKASSMSEVHDEPE-DFISKVFFDCS	404	DR
353	QQQSRASYRIQATRMMTGAGNIKKHAAEQAKKASSMSEVHDEPE-DFISKVFFDCS	412	DR
353	QQQSRASYRIQATRMMTGAGNIKKHAAEQAKKASSMSEVHDEPE-DFISKVFFDCS	412	DR
405	YOCLENCGAVLTLVVRKGSDMSKMYVKDTEGDSANAGADYSEFTEGTVLKPGETOKEF	464	DR
413	YOCLENCGAVLTLVVRKGSDMSKMYVKDTEGDSANAGADYSEFTEGTVLKPGETOKEF	472	DR
465	SVGLIDDDIFEEDEHFVRLSNVLSNIEECBPEEGPAPNSLPLPR-AVLASCPVATI	523	DR
473	RVGJIDDDIFEEDEHFVRLSNVLSNVRVSSEVEDG---TLDNSHVSATACLGSPNTATI	528	DR
524	LDDDHAGITFECOTIHVSESIGMEVKVLTSGARGTVWIPFRUTVEGTAKGGEDEFT	583	DR
529	FDDDHAGITFEEDEHFVRLSNVLSNVRVSSEVEDG---TLDNSHVSATACLGSPNTATI	588	DR
584	YGELEFKNDETVKVLUDEEYERONFFALGERPKWMEGI----SDVTDK-	635	DR
589	LTSKEEERRRIAMGRPIGEHTKVEVITEESTEFKSTVYDPLKLIKNTNLALVGTNSWREQ	708	DR
636	LTMEEBAAKRAEMGKPVLPKEVILEEYESTEFKSTVYDPLKLIKNTNLALVGTNSWREQ	695	DR
649	LTSKEEERRRIAMGRPIGEHTKVEVITEESTEFKSTVYDPLKLIKNTNLALVGTNSWREQ	708	DR
649	LTSKEEERRRIAMGRPIGEHTKVEVITEESTEFKSTVYDPLKLIKNTNLALVGTNSWREQ	708	DR
696	FMEATITVSAAGDEDESEERLRSFCDFYVWHLTUVWKLFACVPPTECHWCAEVN	755	DR
709	PIEATITVSAAGDEDESEERLRSFCDFYVWHLTUVWKLFACVPPTECHWCAEVN	768	DR
756	ILIGMFTIIGDASHFGCTIGKDSYVAVWFAFGTSWPDFTASKAALQDVYDASI	815	DR
769	ILMIGLTTAFIGDASHFGCTIGKDSYVAVWFAFGTSWPDFTASKYATQDQYDASI	828	DR
816	GNVTSNANVFLGLANSVAATIWAQOQEFIVSAGLIAFSVPLFTFAFCISVLY	875	DR
829	GNVTSNANVFLGLANSVAATIWAHANGEQFRVSPGTLAFSFTLFTIAFINGVLY	888	DR
876	RRPHLGEGGGPGRGCKLATTWLVSLWLYLIPATEACYTIGF	921	DR
889	RRRPIEGGEGGPPRATKLJSSLVLLWLYTFFSLEACHCIGF	934	DR
RESULT 9			
09R239	PRELIMINARY:	PRT: 957 AA.	
09R239	AC: 09R239;	DT: 01-MAY-2000 (TREMBREL: 13, Created)	
09R239	DT: 01-MAY-2000 (TREMBREL: 13, Last sequence update)	DT: 01-MAY-2002 (TREMBREL: 21, Last annotation update)	
09R239	DE: Rattus norvegicus (Rat).	DE: Na+-Ca ²⁺ -exchanging protein.	
09R239	OC: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	OC: NCBI_TAXID=10116;	
09R239	RP: SEQUENCE FROM N_A.		
09R239	RC: STRAIN=DABL/RARP S SPRAGUE-DAWLEY;		
09R239	RA: Unl.ap M.T., Bell P.D.;		
09R239	RT: "cDNA cloning of two Na ⁺ /Ca ²⁺ exchangers in mesangial cells from Dali/Rapp salt-sensitive (S) and salt-resistant (R) rats.";		
09R239	RL: Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.		
09R239	DR: EMBL: AF10164; AAD23387; -;		
09R239	DR: InterPro: IPR00364; Ca ²⁺ -beta.		
09R239	DR: InterPro: IPR01623; DnaJ_N.		
09R239	DR: InterPro: IPR004837; NaCa_Exemb.		
09R239	DR: InterPro: IPR004836; Na.Ca_Ex.		
09R239	DR: Pfam: PRO3160; Ca ²⁺ -beta; 2.		
09R239	DR: Pfam: PF01699; Na_Ca_Ex; 2.		
09R239	DR: PRINS: PR01259; NACAEXCHNR.		
Query	4 LRIQPLTSASFHLGICLTVFLFL-----NGLRAEAGGSDGVSTONNECSGSSDCK	55	DR
Query	54 KGVLIPWPKWQDSDFGDKIARATVYFVAMVYMELGVSIADEMSLLEVTSOEKEITIK	113	DR
Query	56 EGVLIPWPKWQDSDFGDKIARATVYFVAMVYMELGVSIADEMSLLEVTSOEKEITIK	115	DR
Query	176 FNMNTIIGCVYVYDGEPRKIKLWRVFTANMSFVWYLYMILAVFSPGQVWMEGL	235	DR
Query	174 FMNMTIIGCVYVYDGEPRKIKLWRVFTANMSFVWYLYMILAVFSPGQVWMEGL	233	DR
Query	236 LTLPFPVCULLAWAKDRKLLFYKYMVKYRTDKHGRILLETEDBPKG--TEMDSK	292	DR
Query	234 LTFFFPPICVVFANVADRLILFKVYKRYRAGKQGMIEHEDRPAKTETEMDSK	293	DR
Query	293 NSH--FLOGNLVPLEGKEDM---ESREMIRTKDKOKHPEKDQDOLIVEANYALS	345	DR
Query	346 HQKSRAFYRIQATRMMTGAGNIKKHAAEQAKKASSMSEVHDEPE-DFISKVFFDCS	404	DR
Query	353 QQQSRASYRIQATRMMTGAGNIKKHAAEQAKKASSMSEVHDEPE-DFISKVFFDCS	412	DR
Query	405 YOCLENCGAVLTLVVRKGSDMSKMYVKDTEGDSANAGADYSEFTEGTVLKPGETOKEF	464	DR
Query	413 YOCLENCGAVLTLVVRKGSDMSKMYVKDTEGDSANAGADYSEFTEGTVLKPGETOKEF	472	DR
Query	524 LDDDHAGITFECOTIHVSESIGMEVKVLTSGARGTVWIPFRUTVEGTAKGGEDEFT	583	DR
Query	529 FDDDHAGITFEEDEHFVRLSNVLSNVRVSSEVEDG---TLDNSHVSATACLGSPNTATI	588	DR
Query	584 YGELEFKNDETVKVLUDEEYERONFFALGERPKWMEGI----SDVTDK-	635	DR
Query	589 CGELEFQDNEVKLITRIFDREEEYKECFSPLVLEPKWIRGMKGFTLNGQPVFRV	648	DR
Query	628 -----ISDVTDK--LTMEEBAAKRAEMGKPVLPKEVILEEYESTEFKSTVYDPLKLI	672	DR
Query	649 HAROHP1STVWSEVDKQPLTSKEEERRIAEMGRPIGEHTKVEVILEEYESTEFKSTVYDPLKLI	708	DR
Query	673 TDKLKKTNLALVGTNSWREQPIEATVSAGEDDDDECGEKPLSCFDYVWHLTVE	768	DR
Query	733 WKVLFACVPTETCHWCAVFSVLTGMLTATGDLASHFGCTIGKDSYVAVWFAFG	792	DR
Query	769 WKVLFACVPTETCHWCAVFSVLTGMLTATGDLASHFGCTIGKDSYVAVWFAFG	828	DR
Query	793 TSVDFDTASKAALQDVYADASIGNVTSNANVFLGLANSVAATIWAQOQEFIVSA	852	DR
Query	829 TSVDFDTASKAALQDVYADASIGNVTSNANVFLGLANSVAATIWAQOQEFIVSA	888	DR
Query	853 GTLAFSVLFTIFAVCISVLYLRRPHLGEGGPRCKLAPTWLVSLWLYLILATL	912	DR
Query	889 GTLAFSVLFTIFAVCISVLYLRRPHLGEGGPRCKLAPTWLVSLWLYLIFSSL	948	DR

Db 601 NDELFKSTQINIDDEEYKNNKFLFLENGEPOLE---MSRKAVILQELGGFVKTR 655
 Qy 636 -----LTMEEREEAKRIAEMCKPVIGEHPKLEVTEES 667
 Db 656 DVVKVQGRDNPPATITSLAERGDEEALKKEERIAEMCKPTLGEHVKEVTEES 715
 Qy 668 YEFKTVKLKIKITNLALWGTWSRDFMEATIVSAGDEDEDSEGERLSCFDYMH 727
 Db 716 YEFKTVKLKIKITNLALWGTWSRDFMEATIVS-SGDDDECGEKLPSCFDYMH 774
 Qy 728 FLIVFWKVLFACTCPTTECHGWCFAVSLILGMLTAIGDLASHFCTIGLKDSTVAV 787
 Db 775 FLIVFWKVLFAFPPTDFTWNGWCFCWVSIIMGLTAIGDLASHFCTIGLKDSTVAV 834
 Qy 788 FVAGFTSPDTESKAALQDVADASIGNVTSNAVNWLGLGANSVAATYWAQOEE 847
 Db 835 FVAGFTSPDTESKAALQDVADASIGNVTSNAVNWLGLGANSVAATYWAQOEE 894
 Qy 848 FHVAGTSLAFSVLFTIFAVFCISVLYRRPFLGEGPRCKLAVTWFSIWIYI 907
 Db 895 FVDPGTLAFSVLFTIFAVFCISVLYRRPFLGEGPRCKLAVTWFSIWIYI 954
 908 LFTALEANCYIKSF 921
 Db 955 VESSLEAYCHVKG 968

RESULT 13

035157 ID 035157 PRELIMINARY; PRT; 940 AA.
 AC 035157;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
 DE Sodium-calcium exchanger.
 GN SLC8A1 OR NCX1.
 OS Mus musculus (Mouse).
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TAXID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RA Shl S., Chang B., Brunnert S.R.;
 RT "Is the Sodium-Calcium Exchanger a Candidate Gene for Mouse Dystrophic
 Cardiac Calcinosis?";
 Submitted (May-1997) to the EMBL/GenBank/DBJ databases.
 EMBL: AB004666; AAC69167.1; -.

MGB; MGT; 107956; Slc8a1.
 InterPro; IPR00364; Calx_beta.
 InterPro; IPR001633; Dnaj_N.
 InterPro; IPR004837; NaCa_Exmembr.
 InterPro; IPR004836; Na_Ca_Ex.
 Pfam; PF03160; Calx_beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMS; TIGR00845; caca; 1.
 DR PROSITE; PS50076; DNAJ_2; 1.
 DR SEQUENCE 940 AA; 10640 MW; 1E6152CAM62899B CRG64;

Query Match 66.5%; Score 3191.5; DB 11; Length 940; Best Local Similarity 67.2%; Pred. No. 1.1e-224; Matches 631; Conservative 108; Mismatches 139; Indels 61; Gaps 10; Qy 4 LRRQPLTSAFLHGLVFLFNLRAEGGSDVPSGTCQNNBSCSSDCHEGVILPIW 63
 Db 2 LRSPLPPVMSMGRFLVALFVSHVHITADEAEGGNETECIGSYCKKGVIPIW 61.
 Qy 64 YPPNPSLGDKTIAVIVVVALTMFLGVSITADRMASIEVTSQERBTIKPNGEST 123
 Db 62 EPQDPSEGDKIKARATVFWAMMFLGVSITADRMASIEVTSQERBTIKPNGEST 121
 Qy 124 TTIRWNEEWSNTLMAQGSSAPEILSLIEVGHGFLAGDGPSTIWSAFAENMFITIG 183
 Db 122 TTIRWNEEWSNTLMAQGSSAPEILSLIEVGHGFLAGDGPSTIWSAFAENMFITIG 181
 Qy 184 ICYVIVPDETRAKHLKHFITAWSFAYWLYMILAVFSPGVQWQWEGLTFFPV 243
 Db 182 LCYVWVPPGETRKHLKHFITAWSFAYWLYMILAVFSPGVQWQWEGLTFFPV 241
 Qy 244 CVLLAWWADDKRLFLYKYMVKYRDKHKGIIETEGDHPKG--IEMDGKMMNH--FL 297
 Db 242 CVVFAWAWDRLFLYKVKYRKGKORGMIIEGDRPASKEIEMDGKVNVHDFL 301
 Qy 298 DGNLUPPLSGKEV---ESREMRIRLKLKOKPERKDLDQIVEMANVYALSHQSKRAF 353
 Db 302 DGALV-LEVEDDRDDEERARERARILKQKHPKEEJELQANTVQUSQOKSRAF 360
 Qy 354 YRQATRMTGAGNLIKKAEDQAKASSMSEVHTDEPE-DISKVFDPSCSYQCLENG 412
 Db 361 YRQATRMTGAGNLIKKAEDQAKASSMSEVHTDEPE-DISKVFDPSCSYQCLENG 420
 Qy 413 AVLITVVRGGDMSTKTMVWDYKTFEDGSANAGADEEFTGTVVLPKGEMOKERSVGTID 472
 Db 421 TVALTMRGGDLSTTFVDFRTEDGIRANAGSDEFTEGTVVLPKGEMOKERSVGTID 480
 Qy 473 IFEDDEHFWRLSNVRLREEQPEGMPPAIFNSPLRRAVIALSPCVATVTDHDHIG 532
 Db 481 IFEDDEHFWRLSNVRLREEQPEGMPPAIFNSPLRRAVIALSPCVATVTDHDHIG 537
 Qy 533 TFECDTIVSSESIGVMEVKVLRSGARGTVVIFPTVEGAKGGEFEDYGELEKND 592
 Db 538 TFECDTIVSSESIGVMEVKVLRSGARGTVVIFPTVEGAKGGEFEDYGELEKND 597
 Qy 593 ETVKTTIRVK--IVDEEYERQENFIALGEPKMNERG----- 627
 Db 598 EIVKTTIVKVIDDEEYENKI-FIEGEPRLEMSEKKALLNELGGFTLGKEMGQP 656
 Qy 628 -----ISDVDRK--LTMEEREEAKRIAEMCKPVIGEHPKLEVTEES 667
 Db 657 IFRKVHARDHP1PSTVITVSEYDDKQPLTSKEDQERIAEMGRPILGEHTKLEVTEES 716
 Qy 668 YEFKTVKLKIKITNLALWGTWSRDFMEATIVSAGDEDEDSEGERLSCFDYMH 727
 Db 717 YEFKTVKLKIKITNLALWGTWSRDFMEATIVSAGDEDEDSEGERLSCFDYMH 776
 Qy 728 FLIVFWKVLFACTCPTTECHGWCFAVSLILGMLTAIGDLASHFCTIGLKDSTVAV 787
 Db 777 FLIVFWKVLFAFPPTDFTWNGWCFCWVSIIMGLTAIGDLASHFCTIGLKDSTVAV 836
 Qy 788 FVAGFTSPDTESKAALQDVADASIGNVTSNAVNWLGLGANSVAATYWAQOEE 847
 Db 837 FVAGFTSPDTESKAALQDVADASIGNVTSNAVNWLGLGANSVAATYWAQOEE 896
 Qy 848 FHVAGTSLAFSVLFTIFAVFCISVLYRRPFLGEGPRCKLAVTWFSIWIYI 907
 Db 897 FKVSPGTLAFSVLFTIFAVFCISVLYRRPFLGEGPRCKLAVTWFSIWIYI 935

RESULT 14

035157 ID 035157 PRELIMINARY; PRT; 595 AA.
 AC 035157;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DE Sodium-calcium exchanger 3 (Fragment).
 GN SLC8A3.
 OS Mus musculus (Mouse).
 OC Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TAXID=10090;
 RP SEQUENCE FROM N.A.
 RA Sokolow S., Heschuelz A., Schurmans S.;

RT "Mus musculus mRNA for sodium-calcium exchanger 3 (NCX3), partial sequence";

RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

RL He Z., Phillipson K. D.;

DR Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; U93214; AAB52920; 1.;

DR MGD; MGI:107976; SIC8a3.

DR InterPro: IPR03644; Ca_x-beta.

DR InterPro: IPR04837; Na_{Ca}-Exemb.

DR InterPro: IPR004836; Na_{Ca}-Ex.

DR Pfam: PF03160; Ca_x-beta; 2.

DR Pfam: PF01699; Na_{Ca}-Ex; 1.

DR SMART; SM0237; Ca_x-beta; 2.

DR TIGRFAMS; TIGR00845; cae; 1.

DR TIGRFAMS; TIGR00845; cae; 2.

FT NON_TER 595 595 AA; 66200 MW; 8EF81CBC6EDB7854 CRC64;

SEQUENCE 595 AA: 66200 MW; 8EF81CBC6EDB7854 CRC64;

Query Match 62.8%; Score 3012; DB 11; Length 595;

Best Local Similarity 97.5%; Pred. No. 7.6e-212; Mismatches 580; Conservative 3; Indels 0; Gaps 0;

Matches 580; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 1 MAWILRLQPLTSALFLHGLVTFVFLNGLRRAEGGSDVPTGQNECSCGSSDCKEGVIL 60

Db 1 MAWILRLQPLTSALFLHGLVTFVFLNGLRRAEGGSDVPTGQNECSCGSSDCKEGVIL 60

QY 61 PIWYPPENPSLGDKJARVIVYFVALTYMEGLGVSLADREVASIEVITSQREVITKKPNE 120

Db 61 PIWYPPENPSLGDKJARVIVYFVALTYMEGLGVSLADREMASIEVITSQREVITKKPNE 120

QY 121 TSTTIRVWNNETWSNLTMALGSSAPEILSLLIEVCGHGRITAGDGLGPSTIVGSAFNMTI 180

Db 121 TSTTIRVWNNETWSNLTMALGSSAPEILSLLIEVCGHGRITAGDGLGPSTIVGSAFNMTI 180

QY 181 TIGICCVYVVPDGETRKIKHLRVFTVTAANSIFATIWLWMLAVFSPGVVQVWEGLTLFF 240

Db 181 TIGICCVYVVPDGETRKIKHLRVFTVTAANSIFATIWLWMLAVFSPGVVQVWEGLTLFF 240

QY 241 FPCVCLLAWADKULFYKMHKRTDHGRTIETEDHPKJIEFMEDKMMNSHFLDN 300

Db 241 FPCVCLLAWADKULFYKMHKRTDHGRTIETEDHPKJIEFMEDKMMNSHFLDN 300

QY 301 LPLEGKEDSERREMIRLKDQKHPKEDQDOLVEMANYALSHQOKSRAFVRIQATR 360

Db 301 LPLEGKEDSERREMIRLKDQKHPKEDQDOLVEMANYALSHQOKSRAFVRIQATR 360

QY 361 MMTGAGNIKKHAEQAKASSMSVHTDEPDEFTSKVFDPCSYOCLENGAVILTVR 420

Db 361 MMTGAGNIKKHAEQAKTSSMSVHTDEPDEFTSKVFDPCSYOCLENGAVILTVR 420

QY 421 KGGGSKTMYDVKYTEDGANGANAGADEFEGTIVLKGEMQEKESVGIIDDDIEEDEH 480

Db 421 KGGGSKTMYDVKYTEDGANGANAGADEFEGTIVLKGEMQEKESVGIIDDDIEEDEH 480

QY 481 FVRLSNVREEEQDEBEGMPAIFNSLPLRRAVLAASPVCATVTLDDDHAGIFTFECDTI 540

Db 481 FVRLSNVREEEQDEBEGMPAIFNSLPLRRAVLAASPVCATVTLDDDHAGIFTFECDTI 540

QY 541 VSEIGMVEMVKLRTSGARCTVTPFRTVEGTAKGGDEFEDTGELEFRNDTV 595

Db 541 VSEIGMVEMVKLRTSGARCTVTPFRTVEGTAKGGDEFEDTGELEFRNDTV 595

RESULT 15

002196 PRELIMINARY; PRT; 892 AA.

AC 002196;

DT 01-JUL-1997 (TREMBrel. 04, Created)

DT 01-JUL-1997 (TREMBrel. 04, Last sequence update)

DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)

DE Na/Ca exchanger.

GN NCX-S01.

OS *Loilio* opalescens (California market squid).

OC *Bukaryota*; *Metazoa*; *Mollusca*; *Cephalopoda*; *Coleoidea*; *Teuthoidea*; *Myopsida*; *Loiliginidae*; *Loilio*.

NCBI_TaxID=31211; OX

Query Match 52.8%; Score 2533; DB 5; Length 892;

Best Local Similarity 57.1%; Pred. No. 1.6e-176; Mismatches 516; Conservative 145; Indels 213; Gaps 30; Gaps 14;

Matches 516; Conservative 145; Mismatches 12; Indels 30; Gaps 0;

QY 23 LFLNGLRAEAGGSDVPTGQNECSCGSSDCKEGVILPIWYPPENPSLGDKJARVIVY 80

Db 14 LFLGLGFDFPFAHASE---DSNDCTCTAETCRNGLIVPRWNPNVGNSGDKLARATV 68

QY 81 FVALYIMEGLGVSLADREMASIEVITSQREVITKKPNE 140

Db 69 FVLMYFLFLGVSLADREMASIEVITSQREVITKKPNE 120

QY 141 LGSSAPEILSLLIEVCGHGRITAGDGLGPSTIVGSAFNMTI 200

Db 129 LGSSAPEILSLLIEVCGHGRITAGDGLGPSTIVGSAFNMTI 180

QY 201 RVFETTAANSIFATIWLWMLAVFSPGVVQVWEGLTLFF 260

Db 189 GVFFITATWSVAFYIWLWLYFLIAVSSYGVVQVWEGLTLFF 247

QY 261 MHKKRTDKRIGLITETEGHPKJEMDGKMMNSHFLDN 320

Db 248 LSKYKTRASKOKGVTQCOEGDAEAGE--GKSEGDALKEGC-DDYEVREFBORKYIETL 304

QY 321 KDLQKHPKEDQDOLVEMANYALSHQOKSRAFVRIQATR 380

Db 305 REMRKNPFLDKMTEADMESEAVRNGPISRAFYIQARLKLTSGNIIKK-ARAQAA 363

QY 381 SSMSEVHTDEPDEFTSKVFDPCSYOCLENGAVILTVRGGDSMTWVUDYKTEDGSA 440

Db 364 QPI-VIDKPEDETRVSFDPGHTVMENGTFTGTVIREGGDLITKLYDVKTEDGTA 421

QY 441 NAGADYEFSTGTVLKGEMQEKESVGIIDDDIEEDEH 498

Db 422 NAGSDQVYVABCTLVYPMETHQKPFISITODDIFEDDEHFTYRISLNRLVGDNSGLPFESQ 481

QY 499 PPAIFNSLPLRRAVLAASPVCATVTLDDDHAGIFTFECDTI 558

Db 482 AEA-----KAQANPFLATVMLDDHAGIFTFECDTI 543

QY 559 RGTIVTPFRTVEGTAKGGDEFEDTGELEFRNDTV 618

Db 534 RGCVKVPHSFVDGTT-YGKDELVDKVDFNDDETEFLRVVUDDETEYKEFFINL 592

QY 619 GEPKUNGRGSDVDTURKLTMEEEKRIALGKPVLGHEPKLEYTIESEFKTVKLI 678

Db 593 DEPYLVKKPGCSSG---SVVSEDDDPVLAELGKPRGENIKTVHIE-TEFKSVKDLI 649

QY 679 KTKTNAALVNGTHSWDQFMEAITSAGDDEDESGEERLPSCEDYMMPLTVFVKLFA 738

Db 650 KKNANISLVGTTSSWEEOFATVVAWEGDDEGEGECKPSMDYIMPFVCLVKLFA 709

QY 739 CVPPEYCHGMCAVFSILIGMILTAIGDLSHFGCTGLKDSVTAFFVAGFTSVPT 798

Db 710 FVPPDLYWGGWACFVSIILIGVLAFTGIGLTFGCTGLKDVATVSEVALGTSVPT 769

QY 799 FASKAALQDVYADASIGNYTGSNAVNLIGLAWVIAIYALQGQPHVSGTAKLRS 858

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